

```

2                               32
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62                               92
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122                              152
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182                              212
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242                              272
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302                              332
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362                              392
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422                              452
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482                              512
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542                              572
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602                               |xxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxx
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|                               692
GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC
ala leu val ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys

722                              752
GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782                              812
CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842                              872
GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

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FIG. 1 (1 of 3)

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902                                     932
GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962                                     992
GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022                                     |xxxxxx ITAM xxxxx|1052
GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082                                     1112
GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142                                     1172
CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202                                     1232
TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262                                     1292
GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322                                     1352
TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382                                     1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442                                     1472                                     |xxxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622                                     1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682                                     1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

|xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

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FIG. 1 (2 of 3)

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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862                                1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922                                1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982                                2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042                                2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102                                2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

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FIG. 1 (3 of 3)

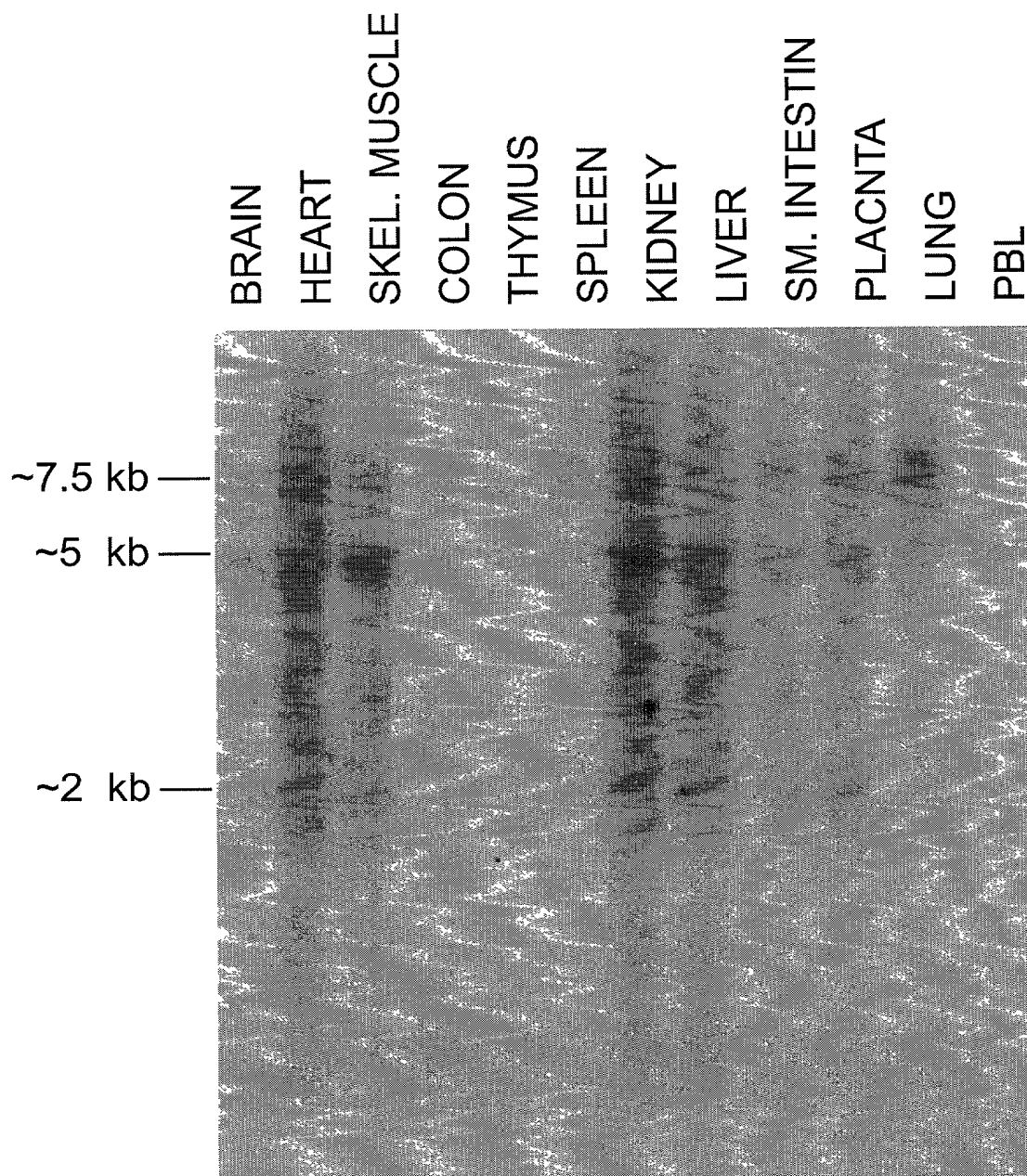


FIG. 2

HC2A
KIAA ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat
HC4
HC1
HC3
HC5

HC2A
KIAA FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat
HC4
HC1
HC3
HC5

HC2A
KIAA KSFARKNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat
HC4
HC1
HC3
HC5

HC2A
KIAA IELPTQLHEKHHLTLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat
HC4
HC1
HC3
HC5

HC2A
KIAA PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat
HC4
HC1
HC3
HC5

HC2A
KIAA QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat
HC4
HC1
HC3
HC5

HC2A	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN
KIAA	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSG--SVR--E
HC5	-----
	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIKSMAQHLENSKVKLIRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMAQHLENSKVKLIRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMAQHLEIDTNKIQLEPQRFPEYQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFEFELMVKSMVHHLYFNDKLEAERKSRFFPERFMDIDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVENLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVQCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPPEYSVTNEF
HC3	RIICSHHYVTLNLPCSLTTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
	Cadherin EC motif
HC2A	CRNHFLVGI LLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRS HQARIAT
KIAA	CRNHFLVGI LLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRS HQARIAT
rat	-----
HC4	CKHHFLVGI LLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQ
HC1	CRKHFLIGI LLREVG FALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGI VLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGI LFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKCVKPEVKVIAA
HC2A	LYLPLFGLLIENVQRINVRDVS?FPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVS?FPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLLENIQRLAGRD TLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPYGMLLDNMPRIY LKDL YPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIA TDDY ESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

FIG. 3A (2 of 5)

HHC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTEGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDLLTYWN-KVSPQELINILILEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFYQMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFYQMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRS-----QTMPALNRNSGVM
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGLTKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSEALKNVFTALRS LIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSEALKNVFTALRS LIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEALKNVFTALRS LIY
HC4	LTVLDTISFFTQCFTKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNF EIGN--NFARVK
HC5	KFGDLLFEEVEQCQFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRPLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3	MQVPMSSLVGTSONFNEEFLRRSLKTLTYAEEDLELRETTFPDQVQDLVFNLMHMLS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILY

FIG. 3A (3 of 5)

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAA	MCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAA	MCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAA	MCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAIHVKNGDFSEAA	MCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAIHARNGDLSEAA	MCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAA	QCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLRLTWLQNMAEKHTKKKCYTEA	AMCLVHA
	SH3	
HC2A	TALVAEYLTRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYLKRKGWYKVEKIC	TASLLSEDTHPCDNSLLTTPSGGSMFSGWPAFLSITPN
HC3	AALVAEYLSMLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLED-----	HSYLPVGSVSFQNISSN
	ITAM	
HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYEITSEISKLIGPI
HC1	IKKEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSERVELIADVKNKPIIAV
HC3	VLEESAVSDDVVPDEEGICSGKYFTESGLVGLLEQAAAFSGMAGMYEAVNEVYKVL	IPI
HC5	VLEESVVSSEDTLSPDEGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVL	IPI
	ITAM ITAM ITAM ITAM	
HC2A	YEKRRD-----	YFRVAFFGQAAQYQFTDSETDVE
KIAA	YEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETHLYDTLHRAYSKVTEVITR-----	AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG-----	TFRVAFYFGQ
HC1	FEKQRDFKKLSDLIYDTHRSYLVKVAEVDVNSEKRLFG-----	TYFRVAFYFGQ
HC3	HEANRDAKKLSTIHGKLQEAFAFSKIVHQSTGWERMFG-----	TYFRVGFYFG-
HC5	LEAHREFRKLTLTHSKLQRAFDSTVNKDH--KRMFG-----	TYFRVGFFG-
	ITAM ITAM	
HC2A	-FFEDEDGKBYIYKEPKLTPLSEISQRLCLKYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKBYIYKEPKLTPLSEISQRLCLKYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKBYIYKEPKLTPLSEISQRLCLKYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEDDGKBYIYKEPKLTGLSEISLRVLYGKFGTENVKIIQSDKVNKELDPKYA	
HC1	GFFEEEDGKBYIYKEPKLTGLSEISQRLCLKYADKFGADNVKIIQDSNVKVNPKDLDPKYA	
HC3	TKFGDLDEQBFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDCKCLDPNKA	
HC5	SKFGDLDEQBFVYKEPAITKLPEISHRLEAFYGCQFGAEFVEVIKDSNPVDCKCLDPNKA	
	ITAM	
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
HC4	HIQVTVYKPYFDDKELTERKTEFERHNISRFVFEAPYTLGKKQGCIEEQCKRRTILT	
HC1	YIQVTVYVTPFFFEKEIEDRKTDFFEMHHNINRFVFETPFTLSGKKHGGVVEEQCKRRTILT	
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFRRKTILT	
HC5	YIQITFVEPYFDYEMKDRVITYFEKNFNLRFRMYTTPFTLEGRPRGELHEQYRRNTVLT	

FIG. 3A (4 of 5)

	Coiled-Coil 1
HC2A	IHCFFPYVKKRIPVVMYQHHTDLNPIEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVVMYQHHTDLNPIEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVVMYQHHTDLNPIEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSV
HC4	SNSFFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAEQLKCSSTVDVMIQLQLKLQGSV
HC1	SHLFFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFPIYIKTRVNVTHKEEIIILTFIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLCGSV
HC5	MHAFPIYIKTRISVIQKEEFVLTFIEVAIEDMKKKTLQLAVAINQEPDAKMLQMVLCGSV

	Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIIQACSI ALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

	Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRA TKFPAHLQRHQ RDTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA
HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDL SK---RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG---KLSS-----P-----
HC5	YQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPEPHVGT CFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----

FIG. 3A (5 of 5)

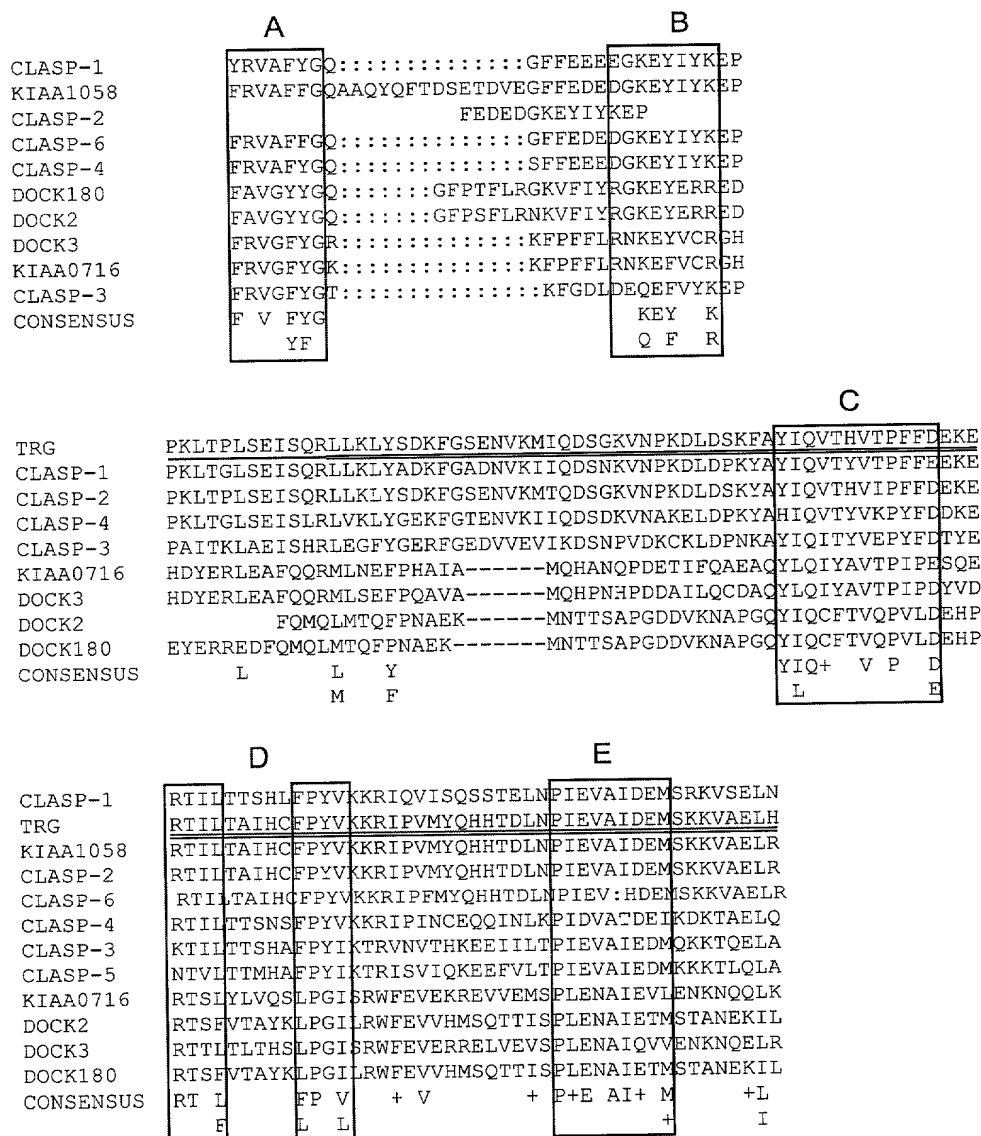


FIG. 3B (1 of 2)

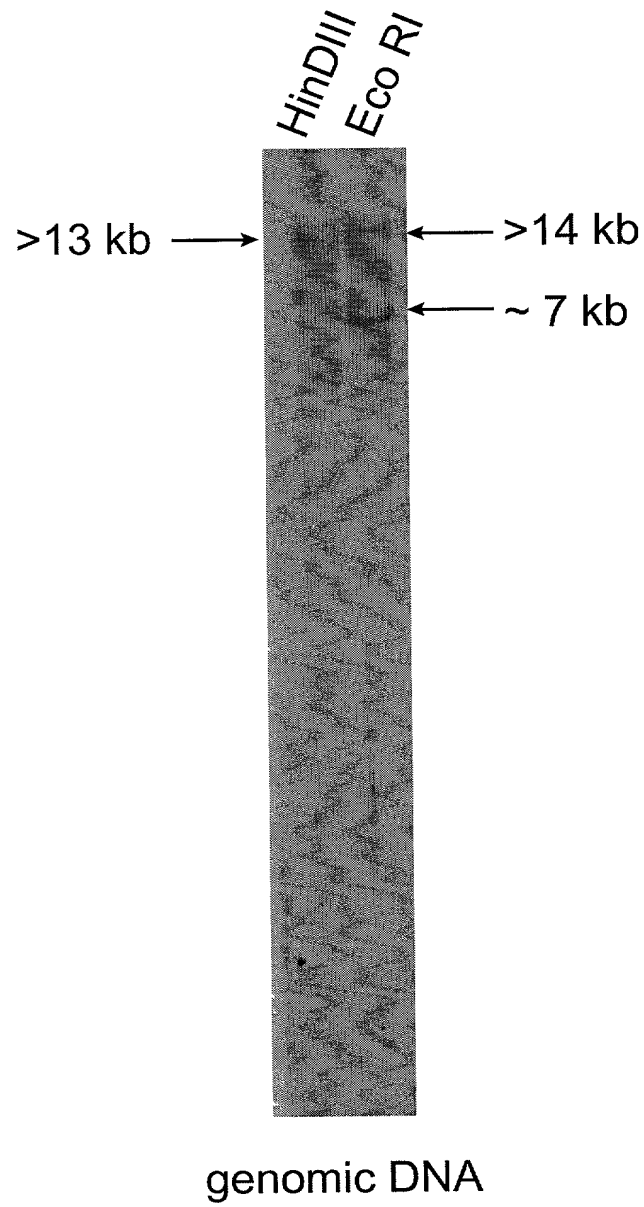


FIG. 4

-12 -1
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG	GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC	CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA	GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC	GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe	glu ile glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG	AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG	GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC	TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC	ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371
TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA	GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
leu lys glu val asp thr ala lys asn lys	glu lys leu glu lys leu arg leu ala ala

FIG. 5A (1 of 6)

1141/381	GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC	1171/391	CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
1201/401	glu gln phe cys thr arg leu gly arg tyr	1231/411	arg met pro phe ala trp thr ala val his
1261/421	TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG	1291/431	CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
1321/441	leu ala asn ile val ser ser ala gly gln	1351/451	leu asp arg asp ser asp ser glu gly glu
1381/461	CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT	1411/471	CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
1441/481	arg arg pro ala trp thr asp arg arg arg	1471/491	arg gly pro gln asp arg ala ser ser gly
1501/501	GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT	1531/511	CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
1561/521	asp asp ala cys ser phe ser gly phe arg	1591/531	pro ala thr leu thr val thr asn phe phe
1621/541	AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG	1651/551	GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
1681/561	lys gln glu ala glu arg leu ser asp glu	1711/571	asp leu phe lys phe leu ala asp met arg
1741/581	CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT	1771/591	CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
1801/601	arg pro ser ser leu leu arg arg leu arg	1831/611	pro val thr ala gln leu lys ile asp ile
1861/621	TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC	1891/631	CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
1921/641	ser pro ala pro glu asn pro his phe cys	1951/651	leu ser pro glu leu leu his ile lys pro
1981/661	TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG	2011/671	GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
2041/681	tyr pro asp pro arg gly arg pro thr lys	2071/691	glu ile leu glu phe pro ala arg glu val
2101/701	TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG	2131/711	CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
2161/721	tyr ala pro his thr ser tyr arg asn leu	2191/731	leu tyr val tyr pro his ser leu asn phe
2221/741	AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT	2251/751	GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
	ser ser arg gln gly ser val arg asn leu		ala val arg val gln tyr met thr gly glu
	GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT		GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
	asp pro ser gln ala leu pro val ile phe		gly lys ser ser cys ser glu phe thr arg
	GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC		AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
	glu ala phe thr pro val val tyr his asn		lys ser pro glu phe tyr glu glu phe lys
	CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC		CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
	leu his leu pro ala cys val thr glu asn		his his leu leu phe thr phe tyr his val
	AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG		GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
	ser cys gln pro arg pro gly thr ala leu		glu thr pro val gly phe thr trp ile pro
	CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC		CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
	leu leu gln his gly arg leu arg thr gly		pro phe cys leu pro val ser val asp gln
	CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC		GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
	pro pro pro ser tyr ser val leu thr pro		asp val ala leu pro gly met arg trp val
	GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG		CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
	asp gly his lys gly val phe ser val glu		leu thr ala val ser ser val his pro gln
	GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG		GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
	asp pro tyr leu asp lys phe phe thr leu		val his val leu glu glu gly ala phe pro
	TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG		GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
	phe arg leu lys asp thr val leu ser glu		gly asn val glu gln glu leu arg ala ser

FIG. 5A (2 of 6)

2281/761	2311/771
CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA	CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG
leu ala ala leu arg leu ala ser pro glu	pro leu val ala phe ser his his val leu
2341/781	2371/791
GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC	CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
asp lys leu val arg leu val ile arg pro	pro ile ile ser gly gln ile val asn leu
2401/801	2431/811
GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT	GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
gly arg gly ala phe glu ala met ala his	val val ser leu val his arg ser leu glu
2461/821	2491/831
GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA	CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
ala ala gln asp ala arg gly his cys pro	gln leu ala ala tyr val his tyr ala phe
2521/841	2551/851
CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG	GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
arg leu pro gly thr glu pro ser leu pro	asp gly ala pro pro val thr val gln ala
2581/861	2611/871
GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC	GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
ala thr leu ala arg gly ser gly arg pro	ala ser leu tyr leu ala arg ser lys ser
2641/881	2671/891
ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG	GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
ile ser ser ser asn pro asp leu ala val	ala pro gly ser val asp asp glu val ser
2701/901	2731/911
CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG	GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
arg ile leu ala ser lys leu leu his glu	glu leu ala leu gln trp val val ser ser
2761/921	2791/931
AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC	GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
ser ala val arg glu ala ile leu gln his	ala trp phe phe phe gln leu met val lys
2821/941	2851/951
AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG	CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
ser met ala leu his leu leu leu gly gln	arg leu asp thr pro arg lys leu arg phe
2881/961	2911/971
CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC	TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
pro gly arg phe leu asp asp ile thr ala	leu val gly ser val gly leu glu val ile
2941/981	2971/991
ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC	GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
thr arg val his lys asp val glu leu ala	glu his leu asn ala ser leu ala phe phe
3001/1001	3031/1011
CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG	GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
leu ser asp leu leu ser leu val asp arg	gly phe val phe ser leu val arg ala his
3061/1021	3091/1031
TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG	TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
tyr lys gln val ala thr arg leu gln ser	ser pro asn pro ala ala leu leu thr leu
3121/1041	3151/1051
CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC	CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
arg met glu phe thr arg ile leu cys ser	his glu his tyr val thr leu asn leu pro
3181/1061	3211/1071
TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC	TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
cys cys pro leu ser pro pro ala ser pro	ser pro ser val ser ser thr thr ser gln
3241/1081	3271/1091
AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC	CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
ser ser thr phe ser ser gln ala pro asp	pro lys val thr ser met phe glu leu ser
3301/1101	3331/1111
GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT	GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
gly pro phe arg gln gln his phe leu ala	gly leu leu leu thr glu leu ala leu ala
3361/1121	3391/1131
CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG	TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
leu glu pro glu ala glu gly ala phe leu	leu his lys lys ala ile ser ala val his
3421/1141	3451/1151
AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC	CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
ser leu leu cys gly his asp thr asp pro	arg tyr ala glu ala thr val lys ala arg
3481/1161	3511/1171
GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG	ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
val ala glu leu tyr leu pro leu leu ser	ile ala arg asp thr leu pro arg leu his

FIG. 5A (3 of 6)

3541/1181	3571/1191
GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser	arg leu ala ser met leu asp ser asp thr
3601/1201	3631/1211
GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile	asn pro ser val ala met ala ile ala gly
3661/1221	3691/1231
GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser	ile ser gln gly pro pro thr ala ser arg
3721/1241	3751/1251
GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser	arg thr leu leu ala cys val leu trp val
3781/1261	3811/1271
CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln	arg trp ala thr asp leu thr leu pro gln
3841/1281	3871/1291
CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu	cys leu ala ala phe glu tyr lys gly lys
3901/1301	3931/1311
AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr	phe lys lys ser leu asp met lys ala arg
3961/1321	3991/1331
CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly	ala arg gln glu met val arg arg ser arg
4021/1341	4051/1351
GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn	val arg trp arg lys ser val thr his trp
4081/1361	4111/1371
AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr	lys asp glu met glu his glu ala leu val
4141/1381	4171/1391
GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu	val val leu asp thr leu glu ile ile val
4201/1401	4231/1411
CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu	ser val leu gly ala val leu lys val val
4261/1421	4291/1431
CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala	leu phe leu gln his gly leu ala thr gln
4321/1441	4351/1451
AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu	leu phe glu glu asp thr glu leu cys ala
4381/1461	4411/1471
GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys	gly ser arg ile ser thr ile arg thr his
4441/1481	4471/1491
GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg	gln asn phe glu ile gly his asn phe ala
4501/1501	4531/1511
CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu	ser ser leu val gly thr thr gln asn phe
4561/1521	4591/1531
AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys	thr ile leu thr tyr ala glu glu asp met
4621/1541	4651/1551
GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln	val gln asp leu met phe asn leu his met
4681/1561	4711/1571
ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu	his gln glu asp pro glu met leu ile asp

FIG. 5A (4 of 6)

4741/1581	4771/1591
CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG	GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
leu met tyr arg ile ala arg gly tyr gln	gly ser pro asp leu arg leu thr trp leu
4801/1601	4831/1611
CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG	GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
gln asn met ala gly lys his ala glu leu	gly asn his ala glu ala ala gln cys met
4861/1621	4891/1631
GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC	CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
val his ala ala ala leu val ala glu tyr	leu ala leu leu glu asp gln arg his leu
4921/1641	4951/1651
CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC	TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
pro val gly cys val ser phe gln asn ile	ser ser asn val leu glu glu ser ala ile
4981/1661	5011/1671
TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG	GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
ser asp asp ile leu ser pro asp glu glu	gly phe cys ser gly lys his phe thr glu
5041/1681	5071/1691
CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA	GCC GGC TAC TTC ACC ATG GGC GGC CTC TAC
leu gly leu val gly leu leu glu gln ala	ala gly tyr phe thr met gly gly leu tyr
5101/1701	5131/1711
GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC	ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
glu ala val asn glu val tyr lys asn leu	ile pro ile leu glu ala his arg asp tyr
5161/1721	5191/1731
AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG	CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
lys lys leu ala ala val his gly lys leu	gln glu ala phe thr lys ile met his gln
5221/1741	5251/1751
AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG	TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
ser ser gly trp glu arg val phe gly thr	tyr phe arg val gly phe tyr gly ala his
5281/1761	5311/1771
TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG	TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
phe gly asp leu asp glu gln glu phe val	tyr lys glu pro ser ile thr lys leu ala
5341/1781	5371/1791
GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC	ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
glu ile ser his arg leu glu glu phe tyr	thr glu arg phe gly asp asp val val glu
5401/1801	5431/1811
ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG	ICC AAG CTT GAC TCA CAA AAG GCC TAC ATC
ile ile lys asp ser tyr pro val asp lys	ser lys leu asp ser gln lys ala tyr ile
5461/1821	5491/1831
CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT	ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
gln ile thr tyr val glu pro tyr phe asp	thr tyr glu leu lys asp arg val thr tyr
5521/1841	5551/1851
TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC	CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
phe asp arg asn tyr gly leu arg thr phe	leu phe cys thr pro phe thr pro asp gly
5581/1861	5611/1871
CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC	AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
arg ala his gly glu leu pro glu gln his	lys arg lys thr leu leu ser thr asp his
5641/1881	5671/1891
GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT	GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
ala phe pro tyr ile lys thr arg ile arg	val cys his arg glu glu thr val leu thr
5701/1901	5731/1911
CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG	AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
pro val glu val ala ile glu asp met gln	lys lys thr arg glu leu ala phe ala thr
5761/1921	5791/1931
GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA	CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
glu gln asp pro pro asp ala lys met leu	gln met val leu gln gly ser val gly pro
5821/1941	5851/1951
ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC	CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
thr val asn gln gly pro leu glu val ala	gln val phe leu ala glu ile pro glu asp
5881/1961	5911/1971
CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG	CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
pro lys leu phe arg his his asn lys leu	arg leu cys phe lys asp phe cys lys lys

FIG. 5A (5 of 6)

5941/1981	5971/1991
TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC	CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC
cys glu asp ala leu arg lys asn lys ala	leu ile gly pro asp gln lys glu tyr his
6001/2001	6031/2011
CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG	CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
arg glu leu glu arg asn tyr cys arg leu	arg glu ala leu gln pro leu leu thr gln
6061/2021	6091/2031
CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA	CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
arg leu pro gln leu met ala pro thr pro	pro gly leu arg asn ser leu asn arg ala
6121/2041	6151/2051
AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC	AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
ser phe arg lys ala asp leu OPA	
6181/2061	6211/2071
CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG	GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
6241/2081	6271/2091
GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC	CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
6301/2101	6331/2111
CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA	TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

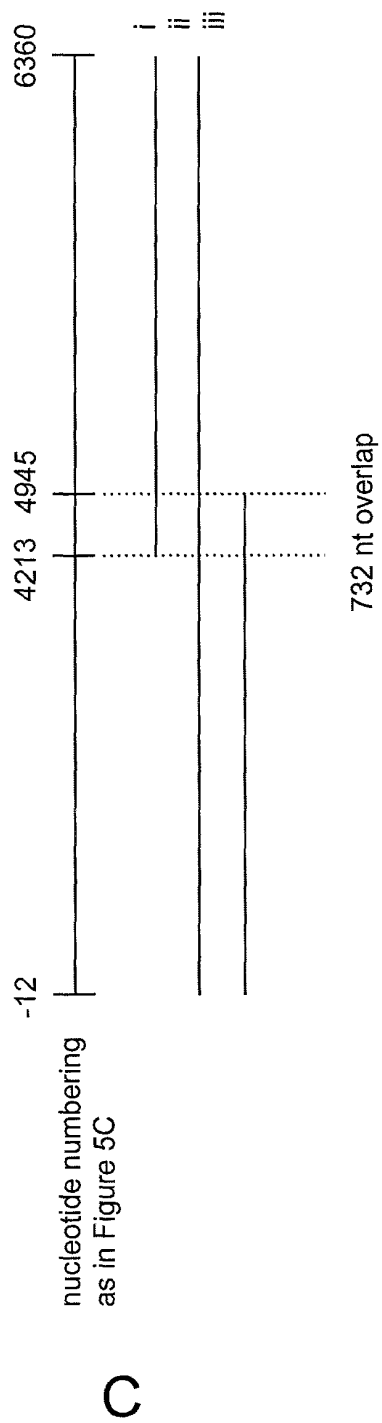
FIG. 5A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5B (2 of 2)



Exon 63800 to 63920

GCGGGGCCGGGGCCCGGGGCGGGCGGGGACGCGAGGACCATGGCTGC
CTCCGAGCGCCGCGCTTCGCGCACAGATCAACAGGTAGTGTGGCCGCGGG
 CCCCCCCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG
CAGGTGTCCCGGAACGCAGTGGCTCCCCCACTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGTAAGTATTTGGGGGTCCGCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTCGAGCCCC
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCGGGCC
CCTCAGGGACCTGGTAGAATTCCAGCTGATGACTTGGAGCTGCTGCTGCAG
CCCCGGGAATGCCGACCACGGAGCCCGGATCCCCAAGGATGAGTGGGTTC
 AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTGCTGCAGAAACTGGATGCCCAGGTGA
GGGCCGCGGTGGAGATGTATATTGAGGACTGGGTTCATTGTCCACAGAAGGTG
 AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCAGCCCCGTTCTCTGCTAGGTATCAGTACCTGAGTGCAGCATACAGC
CCCGTCACACAGACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCGG
 TGAGGAAGCCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAATGACTCCCGCGTGGCTCGGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCTCTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG
AAGATGTGGACCGGCGCAATGAAACCCTTCGACGGCAGCACCGGCCCCCGGC
CCTGCTCACCTCTACCCGGCACCTGACGAGGTGGGTGCCCCCTCCCAGATAT
 CAGCCAACCAGCATTTACT

FIG. 6A (1 of 7)

Exon 78100 to 78250

CCCCGCCAGCTCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCAGAGCCACCCGCGAGCACTTTGGACAAAGGATCTTGGTCAAG
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTTACTTGTAGGTTGAGATTGAAATTGAGCCCATCTTT
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT
TTTTCTCTTCTCCTCC

Exon 80540 to 80750

GTGGTGGCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACTGCCATCTCCACC
CTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCAATTCATCTGCCCCGAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTTGAAAGAAGTGGACAC
AGCCAAGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG
AAGCTGCGCCTGGCGGCCGAGCAGTTCTGCACCCGCTGGGCCGCTACCGCA
TGCCCTTCGCTGGACGGCCGTGCACTTGGCCAACATCGTGAGCAGCGCTGG
GCAGCTGGACCGGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC
AGGCTTGGGGCGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCGCCGCGTCCGGGGCCCCAGGACCGGGCGAGTAGTGGGGACGACG
CCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAACTTC
TTTAAGCAGGTGTCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG
GCGACTACGTCTGTGACTGGTGCGTGGCACACCCCATACACAAGAAGTATC
ACTC

FIG. 6A (2 of 7)

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCCAGGGGCCGGCCACCAAGGAGATTCTGGAGTTCCCCGCC
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCTCTGGGGCCCAGC
TGGGCACTTGA

Exon 87940 to 88130

GCCCCGTGCCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCCAGCCAGGCTCTGCC
GTCAGTGGCTGTGCCCCAGGGAAGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT
AGGGGGACACGTGAGGAACTTGGGGG

Exon 88470 to 88680

GCCCCCAGCAGATCCCCAGCCCGATTCTGCCAGGTCCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTTCCAGCCTGCCGTGACAGAGAACCATCACCTGCTG
TTCACCTTCTACCATGTGAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC
ACCCGTGGGCTTTACTGTGAGCCGTCCCCTCCCTCCCTCCCCCTGAGCCCTCC
T

Exon 88680 to 88870

TCGTCCCCCAACCTGGCCGAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC
CACTGCTGCAGCACGGGCGCCTGAGGACCGGGCCCTTCTGTCTCCCAGTGTCT
GTGGACCAGCCGCCGCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT
TCCGGGCATGCGTGGGTGGACGGTCACAAGGGCGTGTTCAGTGTGGAGCTC
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGGTGGGCCGGGAACCAAGA
GTCCCGCCCTGCTCC

FIG. 6A (3 of 7)

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT
ACCTGGACAAATTCTTCACCCTGGTGACGTCCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG
CGGGCCAGTCTTGCAGCACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT
CTCCCACCACGTGCTGGACAAGCTCGTGCGTCTGGTCATCAGGCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCCTTGGGCCCTGGAACCTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTCACCGGA
GCCTGGAGGCAGCCAGGATGCCCCGCGTCACTGCCCCACAGCTGGCTGCCTA
CGTCCACTACGCCTTTCGCCTTCCTGGCACTGAGCCCAGCCTCCCGGATGGTG
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACTCCATCCTCAGGGGCCCC
TCCAGTGACAGTGACGGCTGCCCACTGGCCCGTGGCTCTGGTCGCCCCGC
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC
GCCGTGGCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA
AGGTAGGGCAACGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC
AGCACGCCTGGTTCTTCTTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG
GTGGCAAGAGACCCCACTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTACCCACCCCAAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC
CGGACGCTTCTTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCCTGGAG
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTGGGTGTGTGGGTGACAGGCACCTGTGTCCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTCTTCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGCTTTGTCTTCAGCCTGGTCCGGGCCCCACTACAAG
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGGCGGA
GC

FIG. 6A (4 of 7)

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCT
CCAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCTGCGCATGGAATTCACCCG
CATCCTGTGCAGCCACGAGCACTACGTGACCCTCAACCTCCCCTGCTGCCCCC
TGTCACCTCCAGCCTCGCCCTCCCCCTCTGTGTCTCCACCACCTCCCAGGTG
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCTTGACCCTGGCATCCCCCATTTTTCCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTTGAAGTGAAGT
GGACCATTCGGGCAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCCC
AGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCTTGAGCACCTCATTACCCCATAGGGCATTCCTG
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTG

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCCGAAGGGG
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCCC
TAGCCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCTCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAATTGACTTTGATTCTCTCTGCCCCAGGCTTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT
GCTGTGGGTGCTGAAAAACACCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT
GACCTGACACTCCCCAGCTGGGACGTCTGTTGGATTGCTGTACCTTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGGGCAGGAGATGATGGAGGAG
GCAGGCTA

FIG. 6A (5 of 7)

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCAGTTCTCTGCACCCCCAGGGGAA
AAAGGCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA
ATGGTTCGGCGAAGTCGTGGTAAGAGGGTGACATACCCACGTGTCCCCATCC
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGCACCCACCGCTCTCAGAGAGGAGCCCCG
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCCGCTGGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCTTGGTGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTTCTGACCCCCCTTCCCTCCAGACGGTGATG
CTTTCAGAAGCCCGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT
ACAGCCTGGGCAGTGCCAGAGTGCCCTCTTCTTGACAGCATGGCCTGGCCAC
CCAGAGGGCCCTTGTGTCCAAGTGAGCACCACTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCCCTGGGGGCAGTTCCCGG
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC
TCGCTGTACCTGCTCATGCGACAGAAGTTCGAGATCGGCCACGTGAGTGGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCGTCCCTGCAGAACTTTGCCCG
TGTGAAGATGCAGGTCACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC
CTGCTGGGTCCCCGCCCGCCTCCCTTCATATAACTCCCAAC

FIG. 6A (6 of 7)

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG
AGGACCCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCCTCCTCACATCCCCCTCACCTGGACTCCAGAATTGCCCGG
GCTACCAGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG
GAAGCACGCGGACGTGGGCAACCACGCCGAGGCCGCCAGTGCAATGGTGCA
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC
CTGCCCCGTGGCTGGCGATTTCCTTCCAGGTGAGTGCCAGGGGTTGGCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGAGTGGGGACCAGGGTCTGACGCCACCTCTCCACCCCAGAACAT
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTGCCCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCCCACCTCACCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCCGGGTGCACGGCAAAGTGCAGGAGGC
CTTCACCAAGATCATGCACCAGGTGGGGCCAGGACCCCCTCCCCAGACCCCA
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCCGGCTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCCTTCTCACAGCCCCAGCGCGT
GTTCCGGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCCTTGTGGTTGGGGGTGGAACGGGGCATGG
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACACGGAGAGATTGGCGACGACGTCGTTGAGATTATCAAAGAC
TCTAACCTGTGGACAAGTC

FIG. 6A (7 of 7)

GGGCATGTGGCTCATTCTGTAAATCCCGGCACTTTGGGAGGCCGAGGCGGGTGGATC
 ACCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC
 TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC
 GGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC
 GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT
 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA
 AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA
 GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTCTGACCAGG
 GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA
 AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGGCTGGAGAATTCTCTAAAAATGCTGC
 AGCAGTGCTGGGAGAGAGGGCCAGTGGGGAGAGATTGAGACCATAGATTAACCAAG
 ACATCCCCACCTCTTCTCTTGGTAGAGCGGCCCGAAAGTCTAGACTCCCAAACT
 GGCTCACTCAGGTCCCAACACCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC
 TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGGCC
 TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT
 ACTCATCTGTAAAAGGAGGAAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGCC
 CAGGCTCAATGACATCTTAGCAATTAGACTTTTGTAGACAGGGTCTCGCTCTGTCAAC
 CAGGCTGGATTGAAATGGCACAAATCACAGCTCACTGCAGCCTTGACCTCCAGGCTC
 AAGCGATCCTCCTCCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA
 TGCCTGGTTAATTTTGCATTTTGTGGACACGGGGTCTCATTATGTTGCCCAGGCT
 GGTCTCCAACCTCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCACAGTGCTGGG
 ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA
 GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC
 CCCCAAACCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCCAGCGCCTCCCCCTCCC
 TCCCTCCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC
 CACTAAACCCCGGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTTCCC
 TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCCAGCTCCCAGGGTGGAAAGAGCGCC
 CCCGCCAGCTCGGGAGTCTGGGGCACCCCACTGCTGGGTCCCAGCGCCTCCTCTCCC
 TAACCTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC
 CCCCCAGCCCGGGAGTCTGGGGCCCCGCCAGCCTGGATCCCGGGGCTCCTCTCCGT
 CCCCAGCCTCAGTTTCCCCAGCCCCCAGGACTCCAGGCGACCCCTCCGGCCTGCAGG
 GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCCGCCCCGCGCCGGCCCCG
 CCCCAGCCCCGGCTGCCAGAACCGGGAGGCGGCGGCGGCGGGCGGGCGGGCCCCG
 GGGCGGCGGCGGGGACGCGAGGACCATGGCTGCCTCCGAGCGCCGCGCCTTCGC
GCACAAGATCAACAGG

FIG. 6B

hCLASP4	-----MFPMEDISISVIGRQRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRVTAAAEVRKQISGQYSGSPQLLKNLNIVG	41
hCLASP2	-----MLLFYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAAEVRKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
	...:	
hCLASP4	-----STVPEDA EKRAQSLFVKECIKTYSTDWHVNVNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAEENLLVKEACKFYSSQWHVNVNYK	120
	:::	
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDLDVVFTFKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRLPNKVVKLDKLPVHVVEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLQPRECRTEP-GIPKD-EKLDAQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPSSHSEIDHEDADKDEDTTS HSSSKGGGGAGGTGVFKSG	180
	::: . : * . : * .	
hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSIYLNLSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKR SMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSND SRRGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT	239
	: : . : : * : : . : .	
hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLA AETE QEME EWLITLKKIIQINTDSL VQEKKETVE	222
hCLASP5	DVSGKGPVTACDFDLRSLQPDKRL ENLLQQVSAEDFEKQNEEARRTN-----RQAE	169
hCLASP3	DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQNDQQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAMQEK	219
hCLASP7	EDTPRSSGASSIFDLRNLAADSLP SLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNLDLYFVLA AETESDMDEWIHTLNRILQISPEGPLQGRRSTEL	299
	:: . : : :	
hCLASP4	TAQDDETSS---QKKAENIMASLERSMHP ELMKYGRETEQLNKL SRGDRQNLF SFDSE	278
hCLASP5	LFALYPSVD---EEDAVEIRPV ECPKEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD---EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD---EQSKLEGSGSGLD SYLPELAKSAREAEIK---LKSESRVKLFYLDPD	272
hCLASP7	LLTLYPAPD---EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE	273
hCLASP1	TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTRNMERLNLFS LDPD	359
	. : : : : : : : :	
hCLASP4	VQRLDFS---GIEPDIKP-FEECKNKRFLVNCHDLTFN ILGQIGDNAKGPP TNVEPFFI	333
hCLASP5	IEPLFAS---IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV	268
hCLASP3	IEPIFAS---LALYDVKEKKKISENFYFDL NSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS---SAEPEVKS-FEEKFGKRI LVKCNDSL SFLNQQCVAENE EGPTTNVEPFFV	327
hCLASP7	IEPIFGI---LALYDVREKKKISENFYFDLNSDSMKGLLRAHGTHPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKKDLLEPESVIKPFEEKAAKRIM ICKALNSNLQGCVTENENDPITNIEPFFV	419
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FIG. 7 (1 of 6)

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLNFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTSNNFIRSKNLLNVE	887
	.. *::** ::. ** : :.	
hCLASP4	EQVMIOQLPVLMLQLFR-----VLTNMTH-----EDDVP	824
hCLASP5	RLEPLVFLHLVLDKLEQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLQSKDQHG	775
hCLASP3	QLEPVVRFLLHLLDKLILLVIRPPVIAGQIVNLGQASFEAMASIIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFAEAMAHVSVLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. : : * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVHYVFRLEPVQRDVPKSGAPTALLDPRSHTYGRISAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAPASLNLNRSRSLSN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQDLH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNCSSRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIIGSKGLDRNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIILAKSM	907
hCLASP5	-----APRPASKKHFFHEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPKTLFHEELALQWVVCSSVRESALQQAFFFFELMVKSM	1019
hCLASP2	-----ADFLTNSKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSASSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * .. : ***	
	Cadherin Cleavage	
hCLASP4	ATYLLLEENKIKLERGQFPETYYHHVLSLLLAIPHVTIRYAEIPDE---SRNVNYSIAS	964
hCLASP5	AQHVHNMDKRDSEFRTFRSDRFMDITTIVNVVTSEIAALLVKPQKENEQAQKMNISLAF	970
hCLASP3	VHHLYFNDKLEAFKRSRFRPERFMDIAALVSTIASDIVSRFQKDETEM---VERLNTSLAF	1076
hCLASP2	AQHILIENSKVKLIRNQRFEPASYHHAAETVVNMLMPHITQKFGDNPEA---SKNANHS LAV	956
hCLASP7	ALHLLLGQRDLTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNLSLAF	999
hCLASP1	AQHLIDTNKIQLERPQRFEPESYQNELDNLMVLSDHVIWKYKDALEE---TRRATHSVAR	1052
	. : : . : * ** . . : : : . . . * : *	
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP----KVLAEYKFEFLQTCNHEHYIPLNL	1019
hCLASP5	FLYDLSLMDRGFVFNLIRHYCSQLSAKLSNL---FTLISMRLFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRILCSHEHYVTNL	1136
hCLASP2	FIKRCFTFMDRGFVFQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNL	1059
hCLASP1	FLKRCFTFMDRGCVFKMVNNYISMFSSGDL----KTLQYKFDLQEVQCQHEHFIPCL	1107
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hCLASP4 NNDGHNPLMKKVFEDIHLAFLKNGQSEVSLKHVFASLRAFISKFPFAFFKGRVNMCAAFY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSSTYLTHCFATLRALIAKFGDLLFEEVEEQCFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAFQALVSKFPPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFVYLCLFQKHQSETALKNVFTALRSLYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQALVSKFPPELLFEEDTELCDLCL 1464
hCLASP1 QCDCQNSLMKRGFDYMLFFQVQNSATALKHVFASLRLVCKFPFAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCSTKISSSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVIIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFNE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
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hCLASP4 SRFQESLFIINNANSRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILYDVTVMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDL 1664
hCLASP2 TRFQQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEEDMGLRSTFAEQVQDLMFNLHMILTDTVMKHEQEDPEMLIDL 1582
hCLASP1 SRFQHSIAITNNFANGDKQMKNSNFPFAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679
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transmembrane

hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGLSEAAAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLTLWLQNMMAEKHTKKCYTEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTLWLQNMAGKHSESRNHAEAAQCLVHSAALVAEYLSMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLDMAKIHVKNGLSEAAAMCYVHVTALVAEYLTRKG----- 1604
hCLASP7 YRIARGYQGSDDLRLTLWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYIALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAAAMCYIHIAALIAEYLKRKGWKVEKI 1739
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hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD---- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVSVSEDTLSPDEGVD 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVIDDVSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD---- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPDCSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD---- 1795
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ITAM

hCLASP4 ---VHYSEEVLLELLEQCVDGLWKAERYEIISEISKLVPIYIEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKIQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAAASFSTGGLYETVNEVYKLVIPILEAHNRDAKKLSTHKGKLE 1813
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYIEKRR----- 1677
hCLASP7 CSGKHFTLGLVGLLEQAAGYFTMGGLYEAIVNEVYKLVIPILEAHRDYKLAAYHKGKLE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSEYELIADVKNPIIAVFEKQDFKLSDIYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM

hCLASP4 AITKILEVMHTKKRLLGTFFRVAFYQSFEEEDGKEYIYKEPKLTGLSEISRLVKIYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFYFG-SKFGDLDEQEFMYKEPAITKLPEISHRLEAFY 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFYFG-IFGDLDEQEFMYKEPAITKLAEISHRLEGFY 1872
hCLASP2 -----DFEDEDGKEYIYKEPKLTPLSEISQRLKLIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYFG-AHFGDLDEQEFMYKEPSITKLAEISHRLEEFY 1791
hCLASP1 SYLKVAEVVNSEKRLFGRYRVAFYQSGFEEEDGKEYIYKEPKLTGLSEISQRLKLIYA 1912
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FIG. 7 (5 of 6)

